

FIG. 1

## Constitutively Active Receptors

File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP I					
MSHR_mouse	melanocyte-stimulating hormone	TMII	92 VSIVLETTIIL K	adenyl cyclase activity/ HEK293, <i>stably transfected</i>	(Robbins, Nadeau et al. 1993)
	MSH				
CLASS A GROUP II					
5H1B_human	5-hydroxytryptamine <sub>1B</sub>	C-terminus of IC3	313 RERKAKTKLGI K, R, Q	binding of [ <sup>35</sup> S]GTP[S] / CHO-KI	(Pauwels, Gouble et al. 1999)
5H2A_human	5-hydroxytryptamine <sub>2A</sub>	C-terminus of IC3	322 NEQKAGKVLGI K	IP production / COS-7	(Egan, Herrick-Davis et al. 1998)
2H2C_rat	5-hydroxytryptamine <sub>2C</sub>	C-terminus of IC3	312 NEDDAGKVLGI L	PI hydrolysis / COS-7	(Herrick-Davis, Egan et al. 1997)

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CLASS A GROUP II					
A1AB_human	$\alpha_{1B}$ -adrenergic alpha 1B-AR	TMDI  junction between TMDIII and IC2	63 FAIVGNILVIL A  142 CAISIDRYIGV A 143 CAISIDRYIGV K	IP / COS-7	(Scheer, Fanelli et al. 1997)
A1AB_human	$\alpha_{1B}$ -adrenergic alpha 1B-AR	junction between TMDIII and IC2	CAISIDRYIGV K	IP / COS-7	(Scheer, Costa et al. 2000)
A1AB_human	$\alpha_{1B}$ -adrenergic	TMIII  carboxyl end of IC3  TMV	128 AVDVLCCTASI F  293 REKKA <del>A</del> KTGLI E  204 EEPFYA <del>L</del> FSSLG V	IP / COS-1  IP arachidonic acid release  IP / COS-1	(Perez, Hwa et al. 1996)  (Hwa, Gaivin et al. 1997)
A1AB_human	$\alpha_{1B}$ -adrenergic	C-terminal IC3	293 SREKKA <del>A</del> KT X=19 different substitutions	PI / COS-7	(Kjelsberg, Cotecchia et al. 1992)
A1AB_human	$\alpha_{1B}$ -adrenergic	C-terminus IC3	288 293 KFSREKKA <del>A</del> KTGLI K H L	PI hydrolysis / rat fibroblast	(Allen, Lefkowitz et al. 1991)
A2AA_human	$\alpha_2$ C10-adrenergic alpha-2AAR	C-terminal IC3 loop	373 (348?) EKRF <del>T</del> FVLAV X=F, A, C, E, K	adenylyl cyclase inhibition / HEK293	(Ren, Kurose et al. 1993)
ACM1_human	muscarinic Hm1  muscarinic acetylcholine M1	C-terminal IC3 loop junction	360 SLVKEKKAARTLS A	PI / HEK(U293)	(Högger, Shockley et al. 1995)
ACM2-human	muscarinic acetylcholine M2	junction of IC3 and TMVI	390 KKVTRTIL1A 1-4 A inserted	IP production, inhibition of cAMP production / COS-7	(Liu, Blin et al. 1996)

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CLASS A GROUP II						
ACM3_rat	m3 muscarinic (rat)	TMVI		507 TWTPYIMVLVNT S	IP / COS-7	(Blüml, Mutschler et al. 1994)
ACM5_human	muscarinic acetylcholine M3	N-terminus to TMII		chimeric composed of m2 1-69 m5 77-445 m2 391-466	β-gal / NIH 3T3	(Burstin, Spalding et al. 1996)
ACM5_human	m5 muscarinic	TMVI		451 459 465 AIIIA EITW TPYNI MVLVST M L H C V S F T	β-gal; radioligand binding / NIH-3T3	(Spalding, Burstin et al. 1998)
ACM5_human	muscarinic acetylcholine M5	TMVI		465 YNIMVLVSTPCDKCV X=V,F,R,K,+more	β-gal; radioligand binding / NIH-3T3	(Spalding, Burstin et al. 1997)
B1AR_human	β <sub>1</sub> -adrenergic	C-terminus		389 RKAFQGLLCCA R	adenylyl cyclase; agonist binding / CHW	(Mason, Moore et al. 1999)
B2AR_human	β <sub>2</sub> -adrenergic	C-terminal IC3 loop		266 272 FCLKEHKALKTGLI SR K A	adenylyl cyclase activation; agonist binding affinity / COS-7 or CHO	(Samama, Cotecchia et al. 1993); (Lefkowitz, Cotecchia et al. 1993)
DADR_human	dopamine D1A	carboxyl terminal IC3		264 SFRMSEKRETKVLKT I K 288 from D1B receptor APDTSIKKETKVLKT	adenylyl cyclase; cAMP accumulation / HEK293	(Charpentier, Jarvie et al. 1996)
DADR_human	dopamine D1	TMVI		286 FVCCWLPFFIL A	CAMP accumulation / COS-7	(Cho, Taylor et al. 1996)
HH2R_rat	histamine H <sub>2</sub>	IC2		115 FMISLDRYCAV N, A	cAMP producti n / HEK-293	(Alewinse, Timmerman et al. 2000)

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP III					
OPSD_human	opsin	TMII	<sup>90</sup> FMVLGGFTSTLY D	transducin; phosphorylation by rhodopsin kinase / COS	(Rim and Oprian 1995)
	rhodopsin	TMIII	113 GCNLEGGFAT Q		
		TMVII	292 296 MTIPAFFAKSAAIY E G, E, M <sup>32</sup> Ala neutral a.a converted to carboxylate and competes with <sup>113</sup> Glu for salt bridge with <sup>286</sup> Lys		
OPSD_human	opsin	TMIII	134 VVLAIERYVVV I, Q, S	transducin; radioligand binding / COS	(Acharya and Karnik 1996)
OPSD_human	rhodopsin	TM6	257 RMVLIIMVIAFL Y, N	transducin, GTP- $\gamma$ S uptake / COS	(Han, Smith et al. 1998)
OPSD_human	opsin	plus TM3 TMVII	plus G113Q 296 PAFFAKSAAIY G X=E, M natural mutants + 10 different a.a. substitutions disrupts critical salt bridge between <sup>286</sup> Lys(TMVII) and <sup>113</sup> Glu(TMIII)	transducin; radioligand binding / COS	(Govardhan and Oprian 1994); (Cohen, Yang et al. 1993)
	rhodopsin	IC2	134 VVLAIERYVVV Q		(Cohen, Yang et al. 1993)

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TRFR_mouse	thyrotropin-releasing hormone TRH-R	carboxyl tail	<sup>335</sup> FRKLGNCKQK STOP	<sup>45</sup> Ca <sup>2+</sup> efflux, [Ca <sup>2+</sup> ] / Xenopus oocytes; IP formation / AIT20, <i>stably transfected</i>	(Matus-Leibovitch, Nussenzveig et al. 1995)

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP IV					
BRB2_human	bradykinin B <sub>1</sub>	TMIII	113 AIIISMNLYSSI A	IP production / COS-7	(Marie, Koch et al. 1999)
	B2 bradykinin BK-2	TMVI	256 LLPFIICWLPFQI F		

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS A GROUP V					
AG2R_rat	AT <sub>1A</sub> Type-1A angiotensin II	TMIII	111 ASVSFNLVASV A disrupts <sup>111</sup> Asn(TMIII) - <sup>111</sup> Tyr(TMVII) interaction	phospholipase C; IP production / COS-7	(Grobowski, Maigret et al. 1997)
AG2R_rat	AT <sub>1A</sub> Type-1A angiotensin II	C-terminus of TM7 other multiple mutations	305 LFYGF <sub>L</sub> GKKFK Q	IP production / HEK- 293; intracellular Ca <sup>2+</sup> mobilization / CHO	(Parnot, Bardin et al. 2000)
FMLR_human	Type-1A angiotensin II formylmethionylleucyl/phenylal- anine (fMLPR)	IC1	51 LVVWVAGFEMTHVTITISYLNKAVA LVVWVTAPEAKRTINAIWFLNLAVA (K above conflicts with SWISS-PROT database)	PI production; phospholipase C stimulation / COS-7	(Amatruda, Dragas- Graonic et al. 1995)
IL8B_human	interleukin-8 receptor B CXCR-2 chemokine	IC2	138 ACISVDRYLAIVH V	IP production; Ca <sup>2+</sup> mobilization and actin polymerization / NIH 3T3	(Burger, Burger et al. 1999)
LSHR_human	luteinizing hormone (LH)	IC3	564 MATNRDTKIACK G	cAMP production / HEK293	(Kudo, Osuga et al. 1996)
LSHR_human	luteinizing hormone (LH)	TMVI	578 ILIFTDTCTMA G	cAMP production / COS-7	(Shenker, Laue et al. 1993)
LSHR_human	luteinizing hormone (LH)	TM6	571 577 KIAKKMAILIFTDTCTM I I	cAMP production / COS-7	(Kosugi, Van Dop et al. 1995)
LSHR_rat	luteinizing hormone / human chorionic gonadotropin (LH/hCG)	TMVI	556 ILIFTDTCTMA G, Y	cAMP production / HEK 293T	(Bradbury, Kawate et al. 1997; Bradbury and Menon 1999)
OPRD_mouse	delta opiod receptor	TM3	128 KVLSDYNNMF A, K, H	adenylyl cyclase inhibition / COS-7	(Cavalli, Babey et al. 1999)
OXYR_human	oxytocin	IC2	137 LMSLDRCCLATC A	IP production / COS-7	(Fanelli, Barbier et al. 1999)

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PAFR_human	platelet-activating factor (PAF)	C-terminus of IC3	231 EVKRRALMMVCTVLAV R	IP production / COS-7	(Parent, Le Gouill et al. 1996)
PAFR_human	platelet-activating factor (PAF)	TMIII	100 CLFFINQYCSV A	arachidonate release, IP production, adenylyl cyclase inhibition / CHO	(Ishii, Izumi et al. 1997)
PE23_human	prostaglandin E <sub>2</sub> , EP3III EP3IV	C-terminal tail	360 FCQEEFWGN FCQMRKRRLRQEEFWGN ↑truncated	inhibition of adenylyl cyclase / CHO-K1	(Jin, Mao et al. 1997)
PE23_mouse	prostaglandin E <sub>2</sub> , EP3	carboxyl-terminal tail	336 KILLRKFCQIRDHT (3α) MMNHL (3β) ↑truncated	inhibition of adenylyl cyclase / CHO, <i>stably expressed</i>	(Hasegawa, Negishi et al. 1996)
THRR_human	thrombin	EC2 loop	259 268 CHDVNETLLEGYYAYY DLKD KDF I	<sup>45</sup> Ca <sup>2+</sup> efflux, PI hydrolysis, reporter gene induction / COS-7	(Nanevicz, Wang et al. 1996)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	EC1  EC2	486 YYNHALDWQTG F, M  568 YAKVSI <del>C</del> LPMD T	inositol phosphate-- diacylglycerol cascade / COS-7	(Parma, Van Sande et al. 1995)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	TMIII  TMVII	509 ASELSVYTLTV A  672 YPLNSCANPFL Y	adenylyl cyclase activation / COS-7	(Duprez, Parma et al. 1994)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	TMV	597 VAFVIYCCCHV L	cAMP formation / COS-7 cells	(Esapa, Duprez et al. 1999)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	TMVII	677 CANPFLYAIFT V	cAMP formation / CHO cells	(Russo, Wong et al. 1999)
TSHR_human	thyrotropin (TSHR) thyroid stimulating hormone	IC3	613 621 VRNPOYNFGDKDTYKIAK deletion	cAMP formation / COS-7	(Wonerow, Schoneberg et al. 1998)



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TSHR_human	thyrotropin (TSHR)	IC3 / TMVI	623 632 KDTKI <sub>A</sub> KRMVLI <sub>I</sub> FTDFICM V I	cAMP activation / COS-7	(Paschke, Tonacchera et al. 1994)
V2R_human	thyroid stimulating hormone vasopressin V2	IC2	136 LAWTL <sub>A</sub> DRHRAI A	cAMP formation / COS-7	(Morin, Cotte et al. 1998)

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS B GROUP I					
CALR_human	human calcitonin hCTR-1 hCTR-2	wild type (native) protein		adenylyl cyclase cAMP production / COS-1	(Cohen, Thaw et al. 1997)
CLASS B GROUP II					
PTRR_human	parathyroid hormone PTH / PTH-related peptide	junction of IC1 and TMII  junction of IC3 and TMVI	223 TRNYIHMLFL R, K  410 KLLKSTLVLM P C, others	CAMP accumulation / COS-7	(Schipani, Jensen et al. 1997)
CLASS B GROUP III					
GIPR_human	glucose-dependent insulinotropic peptide (GIP-R)	TMVI	340 VFAPVTEQAR P	cAMP production / L293	(Tseng and Lin 1997)
GLR_rat	glucagon	junction of IC loop I and TMII  IC end of TMVI	178 TRNYIHGNLFA R  352 RLARSTLTLLIP A	cAMP accumulation / COS-7	(Hjorth, Orskov et al. 1998)
VIPR_human	vasoactive intestinal peptide 1 (VIP)	junction of IC loop I and TMII  junction of IC loop 3 and TMVI	178 RNYIHMLFI R requires functional integrity of the N-terminal EC domain  343 LARSTLTLLIP X= K, P	cAMP production / COS-7 or CHO	(Gaudin, Maoret et al. 1998) (Gaudin, Rouyer-Fessard et al. 1998)

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS C					
CASR_human	calcium-sensing	N-terminal EC	TLSPVAQNKIDSLNIDEECNCSHL various substitutions, in multiple combinations	IP / tsA	(Jensen, Spalding et al. 2000)

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File Name	Receptor	Mutation Site	Sequence	Assay / Cells	Reference
CLASS D					
O74283 RCB2 C. cinereus	pheromone	TM6	229 PLSAYQIYLT P	heterologous yeast assay	(Olesnicky, Brown et al. 1999)
STE2_yeast	pheromone $\alpha$ -factor	TM6	258 QSLVPSIIFI LL	<i>lacZ</i> reporter gene	(Konopka, Margari et al. 1996)
STE2_yeast	pheromone $\alpha$ -factor	double mutations TM5 and TM6	223 MSFVLVVKTLAIR C C 247 251 DSFHLLIMSCQSLL CC CC double mutations shaded double mutations	<i>lacZ</i> reporter gene / yeast	(Dube, DeCostanzo et al. 2000)
STE3_yeast	pheromone $\alpha$ -factor	IC3	194 DVRDILHCTNS Q	$\beta$ -galactosidase	(Boone, Davis et al. 1993)
STE2_yeast	pheromone $\alpha$ -factor	TM6	253 258 LIMSCQSLLVPSIIFI L LP	$\beta$ -galactosidase	(Sommers, Martin et al. 2000)

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FIG. 2

Light Emission Induced by the WT CCK-BR  
vs. a Constitutively Active Mutant

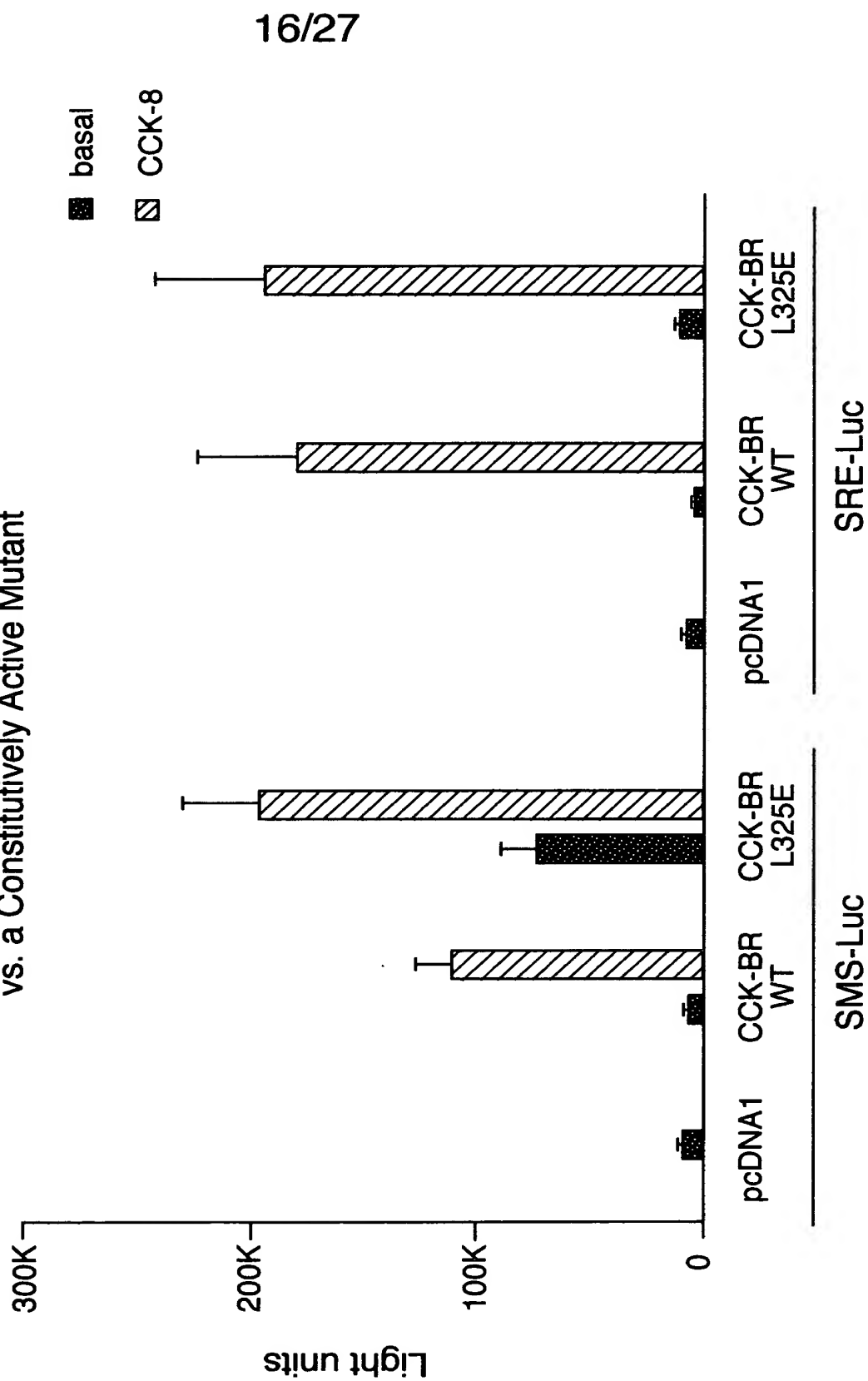




FIG. 3

A Point Mutation Confers Constitutive Activity to the Rat  $\mu$  Opioid Receptor

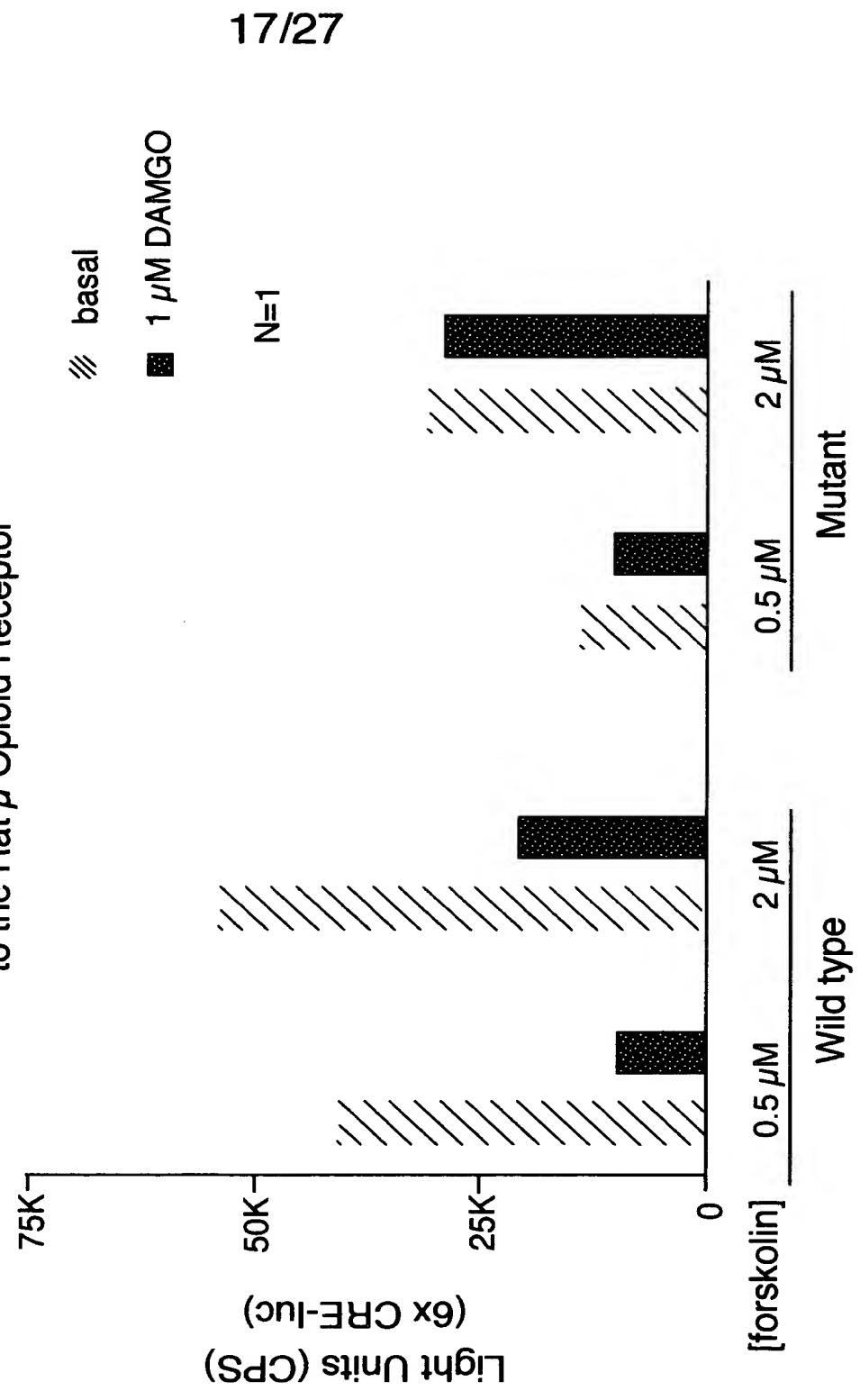


FIG. 4

Forskolin Stimulated HEK293 Cells Transfected  
With pcDNA1 and a CRE-luc Construct

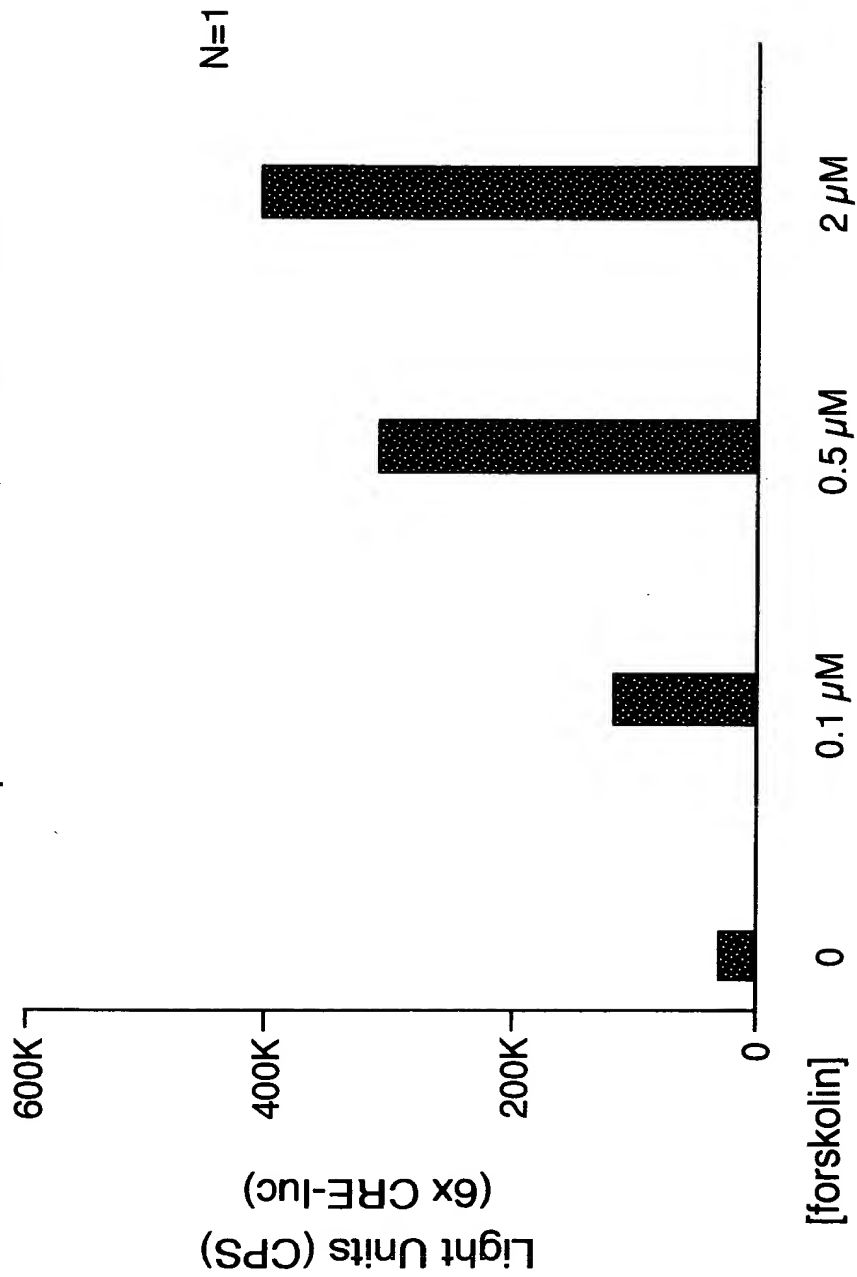
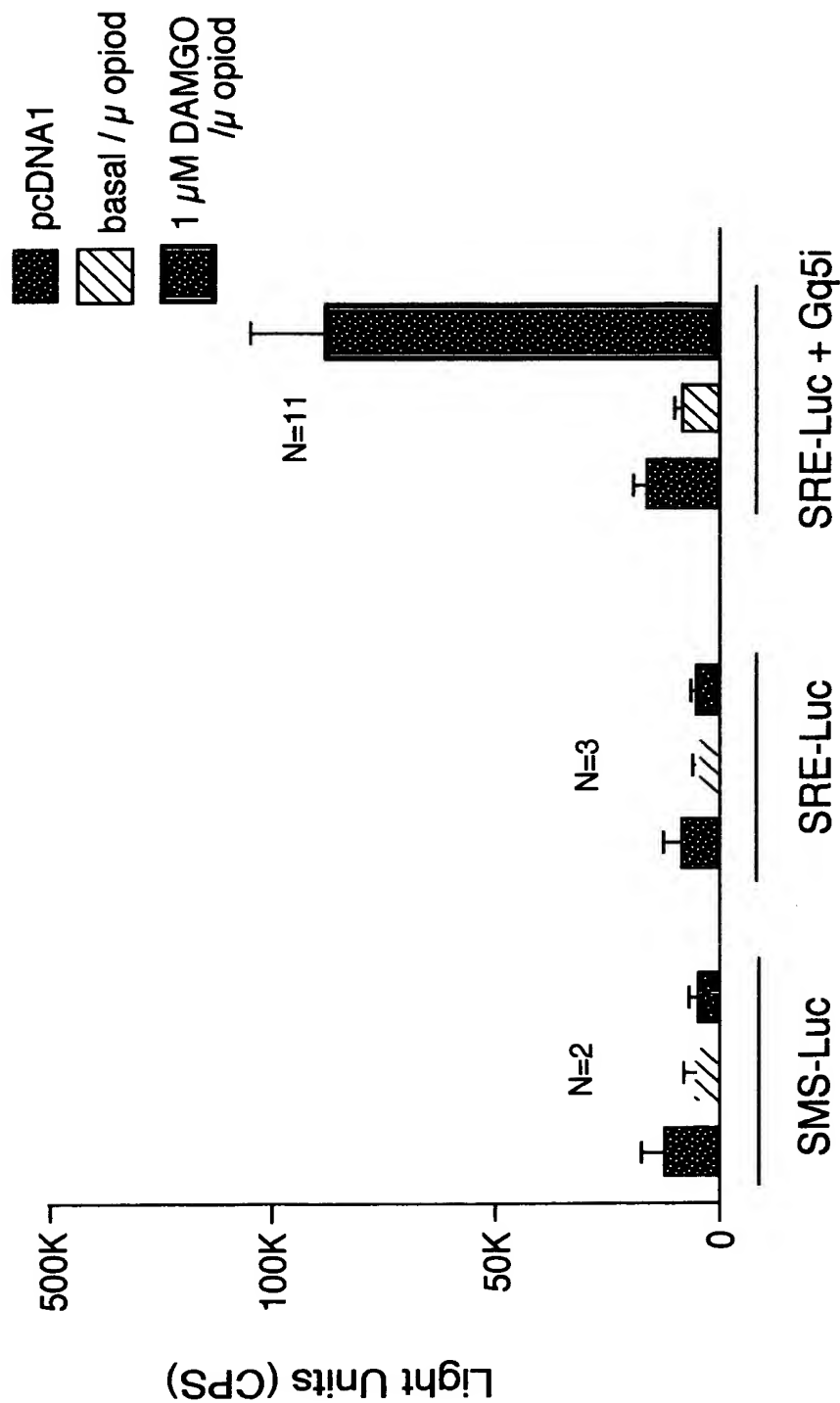


FIG. 5

The Rat  $\mu$  Opioid Receptor Signals Through Gai



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FIG. 6

A Point Mutation Confers Constitutive Activity to the Rat  $\mu$  Opioid Receptor

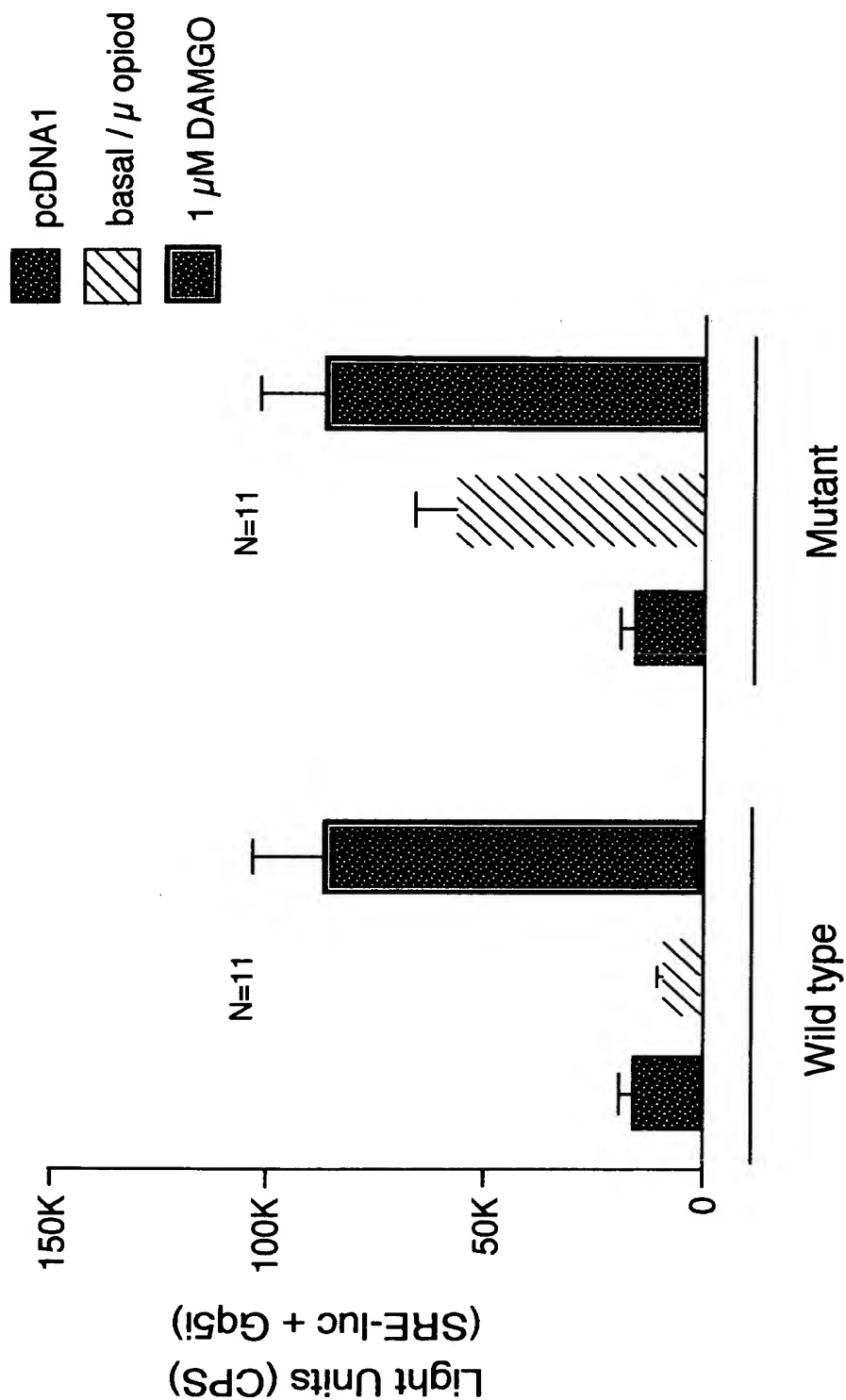


FIG. 7

Target Residues Within Class I GPCR's

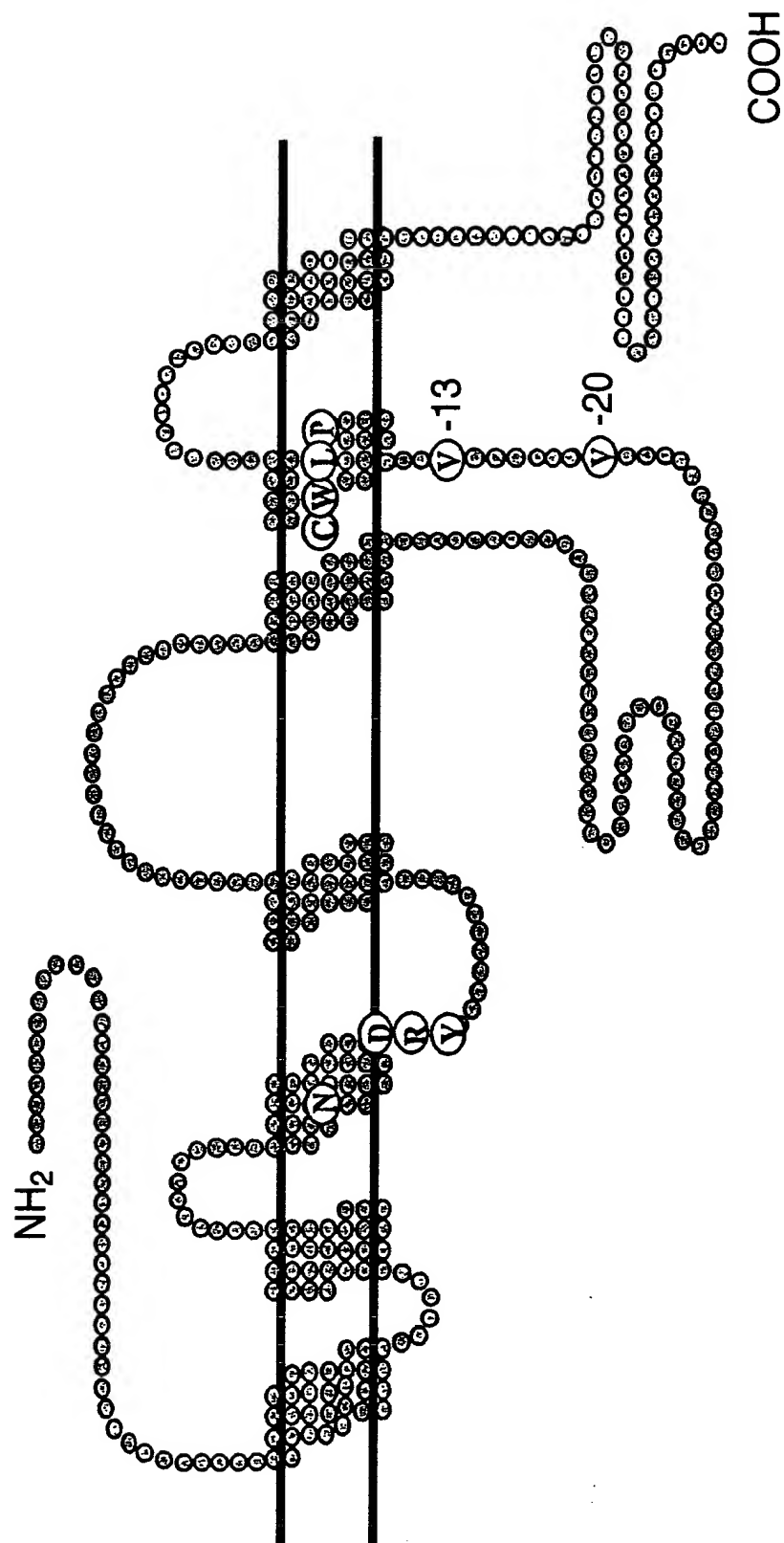


FIG. 8

TMD III Asn (-14 from DRY) is a Target  
for Mutation Induced Constitutive Activity

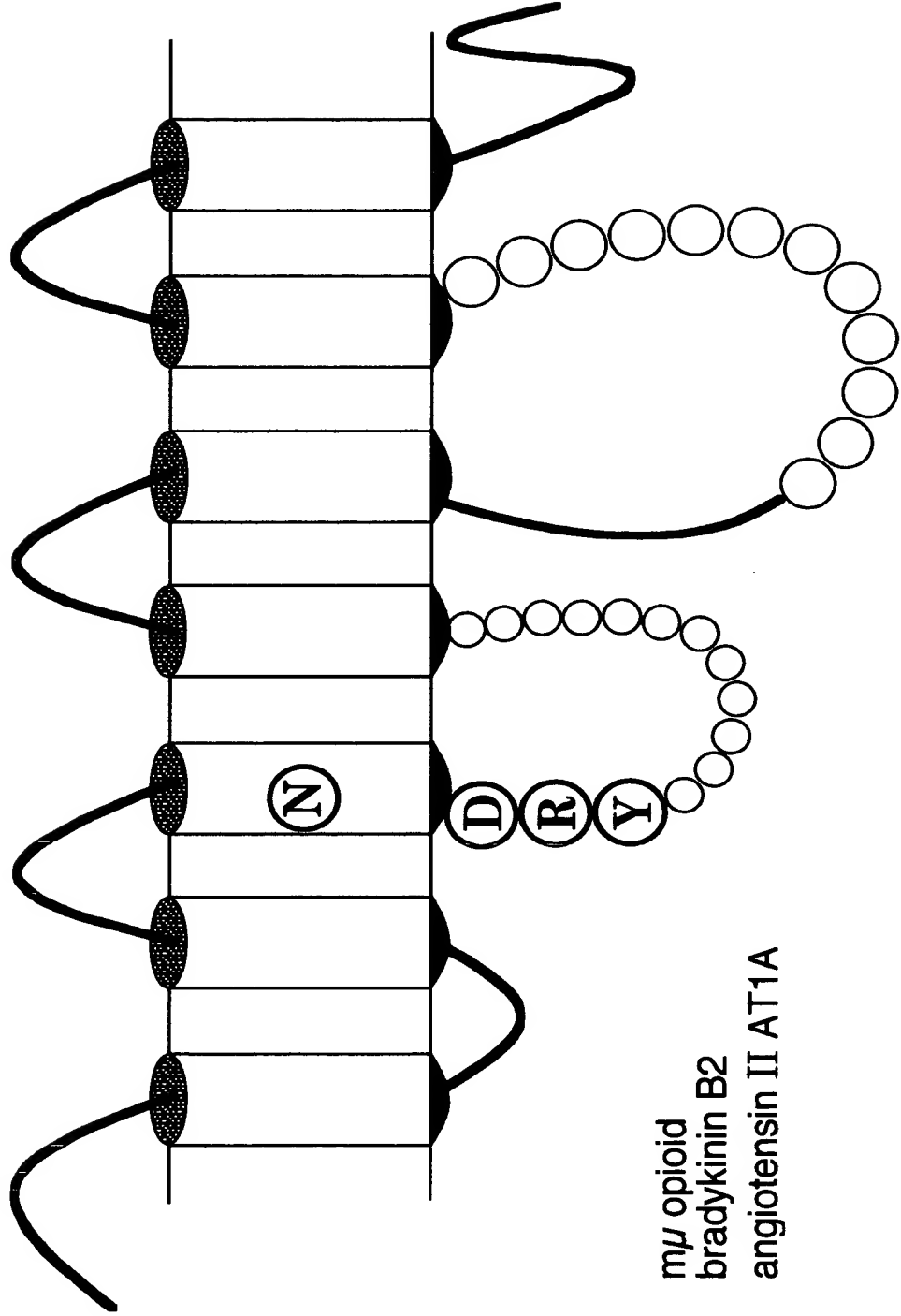


FIG. 9

The 'DRY' Motif is a Target for Mutation  
Induced Constitutive Activity

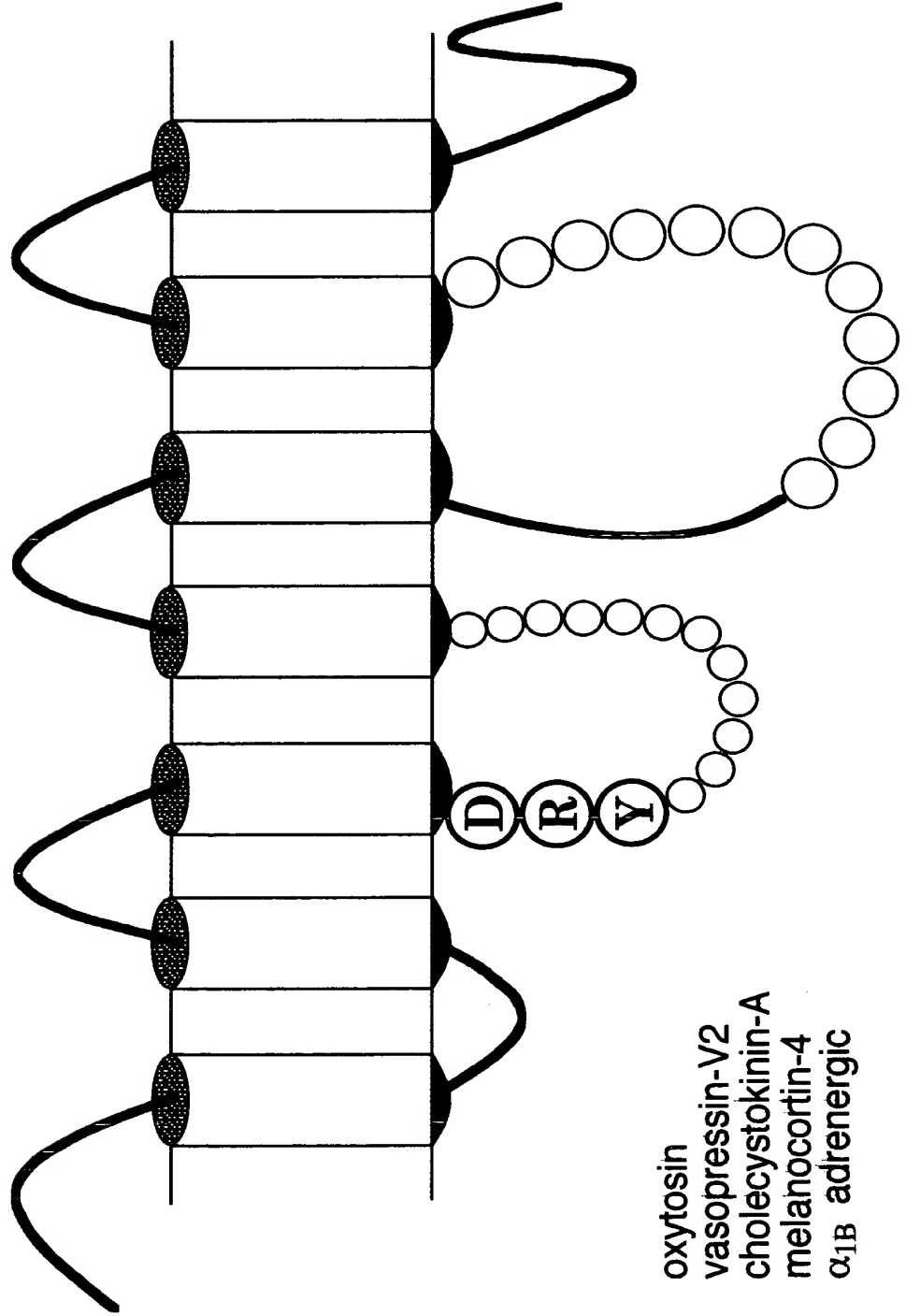


FIG. 10

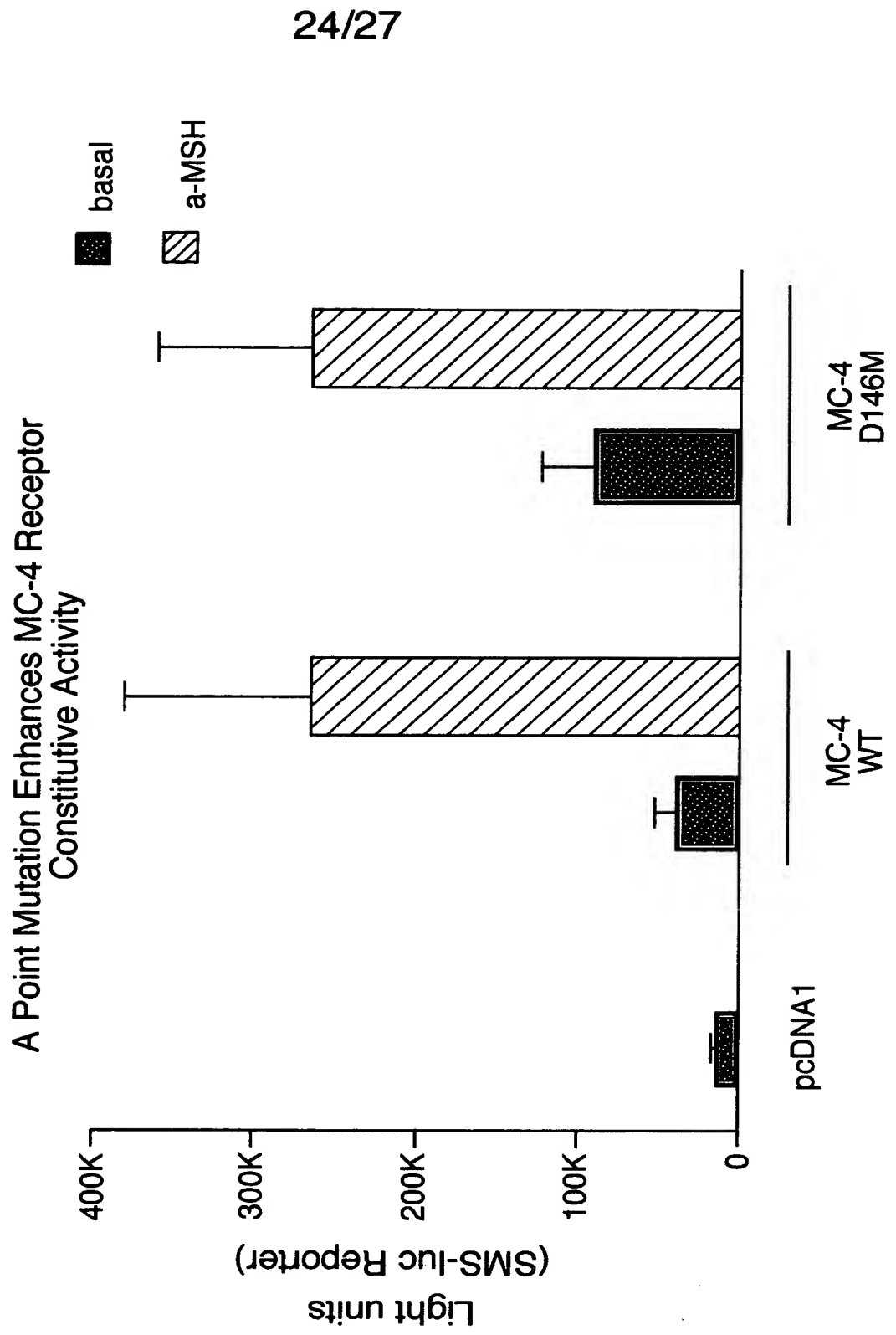




FIG. 11

The -13 Position is a Target for Mutation  
Induced Constitutive Activity

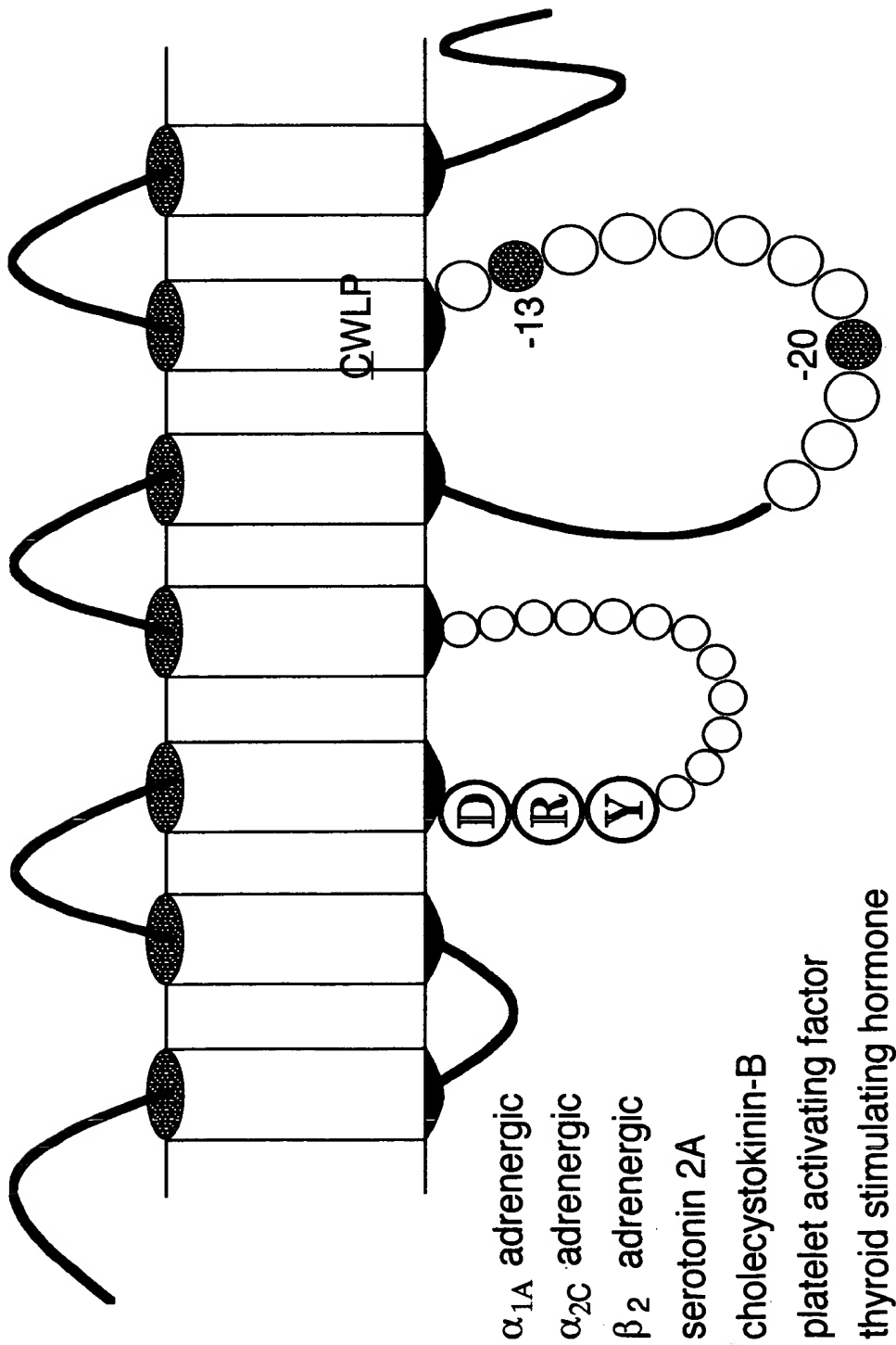


FIG. 12

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ork      1 -----MESI   FRGEPGPTCAPSACLPNNSAWFPGWAEF   INGSAGSSEDAQ
orkr     1 -----MESPIQIFRGEPGPTCAPSACILPNSSSWFPNWAES.   DSNGSVGSSEDOQ
orm      1 MDSSAAPTNASNCTDAAYSSCS PAPS PGSW.   NLSHLDGNLSIDPCGPNRTDLGGGRDSL
ormr     1 MDSSTGPGNTSDCSDPLAQASCPA.   PGSW.   NLSHVDENOSDPCGLNRTGLGNDLSL
ord      1 -----MEBAPSAGAEI.   C. PPLFNASDAYPSACPSACANASG
AT1a     1 -----MALNSSAEDGIKRIQ
BK-2     1 -----MFSPWKISMFLSVREDSVPTTASFSADMLNVTLOQPTLNG.   TFAQ

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ork      49 LEPAEISPAI.   PVBITAYSVVGVGLVGNLSLVMEVIRYTKMKTATNIYIFNLALADA
orkr     49 LEPAEISPAI.   PVBITAYSVVGVGLVGNLSLVMEVIRYTKMKTATNIYIFNLALADA
orm      59 CPPTGS.   PSMITAITIMALLYSHVVCVGLFGNFLVMVIVIRYTKMKTATNIYIFNLALADA
ormr     57 CPPTGS.   PSMVTAITIMALLYSHVVCVGLFGNFLVMVIVIRYTKMKTATNIYIFNLALADA
ord      37 PPGARSASSALARAITALYSAVCAVGLFGNFLVMVIVIRYTKMKTATNIYIFNLALADA
AT1a     16 DDCPRAGRHSYIFVTHPTDYSIEFVVCVFGNLSLVVIVYFYFMCKKIVASVFLNLALADL
BK-2     45 SKCPQVEWLGLWLNTHQPPFLWVFEVETENIFVLSVFLCHKSSCTVAEIVYGNLAAADL

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ork      107 LVTHITPFOSTVYLMN.   SWPFGDILCKIVISIDYNNMFTSIFTLTMSVDRYTAVCHPVK
orkr     107 LVTHITPFOSTVYLMN.   SWPFGDILCKIVISIDYNNMFTSIFTLTMSVDRYTAVCHPVK
orm      118 LATSTLPFOSTVNYLMG.   TPWFGTHLCKIVISIDYNNMFTSIFTLTMSVDRYTAVCHPVK
ormr     116 LATSTLPFOSTVNYLMG.   TPWFGTHLCKIVISIDYNNMFTSIFTLTMSVDRYTAVCHPVK
ord      97 LATSTLPFOSTVNYLME.   TPWFGTHLCKIVISIDYNNMFTSIFTLTMSVDRYTAVCHPVK
AT1a     76 CFLLLPLWAVYTAMEYRWPFGNHLCIASASVTENTYASVELLHCLSDRYATVHIDPK
BK-2     105 ILACGLPFWAITISNNFDLLEGETLORVNAHISMNAYSSICFEMLVSDRYATVHIDPK

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-14 from DRY

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ork      166 ALDERTPLKAKIENICIWHLSSVGLSAYVLCGKVR.   EDVDVIECSLOFPDDDYSEWD
orkr     166 ALDERTPLKAKIENICIWHLSSVGLSAYVLCGKVR.   EDVDVIECSLOFPDDDYSEWD
orm      177 ALDERTERNAKIENYONWHLSSAICHENFMATIKYR.   Q.   GSILCHLTSHPTW.   YWE
ormr     175 ALDERTERNAKIENYONWHLSSAICHENFMATIKYR.   Q.   GSILCHLTSHPTW.   YWE
ord      156 ALDERTPAKAKIENICIWHLASGVCPHVMVIRPR.   D.   GAVVOMLOFFSPSW.   YWD
AT1a     136 SRLRRLMLVAKYTCIIHWMAGLASIPAVIHRNV.   YFIENTNITVCAFHYESRN.   STLP
BK-2     165 MGRMRGVRWAKYSEVITGCTLLSSPMTVFRMTKEYSDEGHNVATCVLSVPS.   LIME

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ork      224 LFMKICVFIFAFTVPVLLIHVCYTMILRLKSVRLSGSSEKDRNLRRITRVLVVAVF
orkr     224 LFMKICVFIFAFTVPVLLIHVCYTMILRLKSVRLSGSSEKDRNLRRITRVLVVAVF
orm      232 NLKICVFIFAFTVPVLLITVCYGLMLRLKSVRLSGSSEKDRNLRRITRVLVVAVF
ormr     230 NLKICVFIFAFTVPVLLITVCYGLMLRLKSVRLSGSSEKDRNLRRITRVLVVAVF
ord      211 TVTKICVFIFAFTVPVLLITVCYGLMLRLKSVRLSGSSEKDRNLRRITRVLVVAVF
AT1a     193 IGLGLTKNILGELFPFLBELTSYVNLWKALKKAYEIQKNIPND.   IFREDAIVLFE
BK-2     222 VFTNMLLNWVGEELP.   LSVITFCITVHVOVLRRNNEMOKFKEIQTE.   RRATVIVLVVLLLF

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ork      284 IVCWTPIHIFVEALGS.   T.   SHSTAALSSMYFCIALGYTNSSINPVLVYAFLDENF
orkr     284 IHCWTPIHIFVEALGS.   T.   SHSTAALSSMYFCIALGYTNSSINPVLVYAFLDENF
orm      292 IVCWTPIHIFVEALKALVTP.   E.   HIFQTVSMEFCIALGYTNSSINPVLVYAFLDENF
ormr     290 IVCWTPIHIFVEALKALVTP.   E.   HIFQTVSMEFCIALGYTNSSINPVLVYAFLDENF
ord      271 VVCWAPIHIFVVTLDID.   RRDPLVVAALHLCHALGYANSSINPVLVYAFLDENF
AT1a     250 FFSVVEHQLETFLLVLLQGVHDCIKSIDIVDTAMPITICLAYFNNCLNPLFYGLGKKE
BK-2     280 IHCWLEFQISTFILLTHRLGILSSCODERIIDVITQIASFMAYNSNCLNPLVYVIVGKRE

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SEQ ID NO:

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orkr     338 KRCFRLECFPLKMRMEROSTSRAR.   NTVQD.   PASMROVGGYNKPV----- 77
orm      346 KRCFRLECFIPTSSNIEOONSURVRONT.   RDHPSLANTVDRTNHOLENLEAETAPLP 78
ormr     344 KRCFRLECFIPTSSNIEOONSURVRONT.   RDHPSLANTVDRTNHOLENLEAETAPLP 79
ord      326 KRCFRLOLCKPCGRPDPSFSRAREATAREVRTACTPSDGPGGGAAA----- 80
AT1a     310 KRYELQLLYPPKAKSHS.   SLSTKM.   STLSTYRPSDNSSSSAKKPASCFEVE- 81
BK-2     340 RKKSWEVYQGVCKRGGCRSEPIOMENSM.   GTL.   RTSISVERQNHKLQDWAGSRQ 82

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0966871.031202

FIG. 13

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mORmouse 1 MDSSAGEGNI SDOSDPIA . FASCSPA . ECSTWML SHADGMS SDPOGPNRTGLGGSKSLC  
 mORrat 1 MDSSGTGGNTSDOSDPIA . OASCSPA . ECSTWML SHADGMS SDPOGPNRTGLGGSKSLC  
 mORbovin 1 MDSCAVPTNANCNCHDEFTHPSSCSPAPSESSONANF SHLEGML SDPOGPNRTGLGGSKSLC  
 mORhuman 1 MDSSAAPTNAACNDALAY . SSCSPAPSESSONANF SHADGMS SDPOGPNRTGLGGSKSLC  
 mORpig 1 MDSSADERNANCNCHDEFSPSSMCSPVPSESSONANF SHLEGML SDPOGPNRTGLGGSKSLC  
 mORws 1 MSHS...GNISOFLYPLS.....NPVMS.....NSSVLCRNFSTSTSFNMGSSRDSTD  
 AT1a 1 -----MALNSSAEDGKRIQDDG  
 BK-2 1 -----MFSEWKISMFLEVRSDSVPTTASFSAFMLNVTLOGETLNG . TFACSKG

mORmouse 58 POTGSPSMITAITIVALYSIVCVWGLFGLNPLVMYIVRYTKTKPATNIYIENLALADALA  
 mORrat 56 POTGSPSMITAITIVALYSIVCVWGLFGLNPLVMYIVRYTKTKPATNIYIENLALADALA  
 mORbovin 61 ESAGSPSMITAITIVALYSIVCVWGLFGLNPLVMYIVRYTKTKPATNIYIENLALADALA  
 mORhuman 60 PPTGSPSMITAITIVALYSIVCVWGLFGLNPLVMYIVRYTKTKPATNIYIENLALADALA  
 mORpig 61 PPTGSPSMITAITIVALYSIVCVWGLFGLNPLVMYIVRYTKTKPATNIYIENLALADALA  
 mORws 48 EODKLE . VIIAIIHTTLYSIVCVWGLFGLNPLVMYIVRYTKTKPATNIYIENLALADALA  
 AT1a 19 EKAGRHSYIFVM . IPTLYSIVCVWGLFGLNPLVMYIVRYTKTKPATNIYIENLALADALA  
 BK-2 48 PQVEWLWENTII . QPPFLWVLFVETLENI FVLSVFLHKSSQIVAEIVLGNLAAAEILIL

mORmouse 118 TSTLPEFSVNYLMG . TWPEGNILCKIVLSIDYNNMFTSIFTLCTMSVDRYIACHPVKAL  
 mORrat 118 TSTLPEFSVNYLMG . TWPEGNILCKIVLSIDYNNMFTSIFTLCTMSVDRYIACHPVKAL  
 mORbovin 121 TSTLPEFSVNYLMG . TWPEGNILCKIVLSIDYNNMFTSIFTLCTMSVDRYIACHPVKAL  
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 mORpig 121 TSTLPEFSVNYLMG . TWPEGNILCKIVLSIDYNNMFTSIFTLCTMSVDRYIACHPVKAL  
 mORws 107 TSTLPEFSVNYLMG . TWPEGNILCKIVLSIDYNNMFTSIFTLCTMSVDRYIACHPVKAL  
 AT1a 78 LLTLELWAVYTAMEYRTPFGNHLCKIASASVTENYASVELTCTPSIDRYIACHPVKAL  
 BK-2 107 ACCLEPEWATITISNNFDWLEGETLORVNAII SMNLYSSICFEMLVSTEDRYIACHPVKAL

mORmouse 177 DFRTPRNAKIMVNCNWLSSAIGLPVMEFMATTKYRC.....GSIDCTLTFESHPTWYWE  
 mORrat 177 DFRTPRNAKIMVNCNWLSSAIGLPVMEFMATTKYRC.....GSIDCTLTFESHPTWYWE  
 mORbovin 180 DFRTPRNAKIMVNCNWLSSAIGLPVMEFMATTKYRC.....GSIDCTLTFESHPTWYWE  
 mORhuman 179 DFRTPRNAKIMVNCNWLSSAIGLPVMEFMATTKYRC.....GSIDCTLTFESHPTWYWE  
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 mORws 166 DFRTPRNAKIMVNCNWLSSAIGLPVMEFMATTKYRN.....GSIDCTLTFESHPTWYWE  
 AT1a 138 LRRTMLVAKTCHIIWLMAGLASLPAVHRNV.....YFIENTNITVCAFHESRNSTLP  
 BK-2 167 RMRGVFWAKLYSLVINGCILLSSPULVFRDM.....EYSDEGHNVTAQVTSYPS..LIVE

mORmouse 230 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRNLVVVAVE  
 mORrat 230 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRNLVVVAVE  
 mORbovin 233 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRNLVVVAVE  
 mORhuman 232 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRNLVVVAVE  
 mORpig 233 NLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRNLVVVAVE  
 mORws 226 TLLKICVFIFAFIMEVLLITVCYGLMILRLKSVRMLSGSKEKDRNLRRITRNLVVVAVE  
 AT1a 193 IGLGLTKNLLGSEFELILTSYTLWKAALKAYETQKNKPRMD...DFRTPNAEVLFE  
 BK-2 222 VFTNMLNIVGGLLE . LSHITFCTYKHKVLRNNEYOKFKEIOTE . RRATVNLVWVLLFE

mORmouse 290 IVCWTPPIHYVLIKALITI.....PETTEQIVSWHFCIALGYTNSCLNPVLYAFIDENE  
 mORrat 290 IVCWTPPIHYVLIKALITI.....PETTEQIVSWHFCIALGYTNSCLNPVLYAFIDENE  
 mORbovin 293 IVCWTPPIHYVLIKALITI.....PETTEQIVSWHFCIALGYTNSCLNPVLYAFIDENE  
 mORhuman 292 IVCWTPPIHYVLIKALITI.....PETTEQIVSWHFCIALGYTNSCLNPVLYAFIDENE  
 mORpig 293 IVCWTPPIHYVLIKALITI.....PETTEQIVSWHFCIALGYTNSCLNPVLYAFIDENE  
 mORws 286 IVCWTPPIHYVLIKALITI.....ENSLFQIVSWHFCIALGYTNSCLNPVLYAFIDENE  
 AT1a 250 FFSVPHOISTFDVLIOGVHDCIKSDIVDTAMPITICLAYENNCLNPVLYAFIDENE  
 BK-2 280 IECWLPFOISTFDLTHREGILSSCOBERIIDMITQIASFMAYSNSCLNPVLYAFIDENE

SEQ ID NO:

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 mORbovin 347 KRCFREFC...IPTSSSTIEQONSARIRONTRHPSTANTVDRTNHOLENLEAETAPLF 84  
 mORhuman 346 KRCFREFC...IPTSSSTIEQONSARIRONTRHPSTANTVDRTNHOLENLEAETAPLF 85  
 mORpig 347 KRCFREFC...IPTSSSTIEQONSARIRONTRHPSTANTVDRTNHOLENLEAETAPLF 86  
 mORws 340 KRCFREFC...VPSPSVLDLONSTRNSNPQCEGOSCHKVDNRNRQV----- 87  
 AT1a 310 KVFLELLKYIPPKAKSHS...SLSTKMSLSYRPSDMSSSARKPASCFEVE---- 81  
 BK-2 340 RIKSWEVYOGVCKGGRSEPIOMENSMGTL...RTSISVERQIHKLODWAGSRQ---- 82

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